

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:09:14 ; Search time 299.73 Seconds
(without alignments)
26,982 Million cell updates/sec

Title: US-09-331-631a-3_COPY_117_185
Perfect score: 384
Sequence: 1 NRORPQOQYEQCQERCRH.....EEQREDEKYEERKEEDN 69

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_15: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	384	100.0	666	10 Q9SP14	Q9SP14 macadamia l
2	367	95.6	666	10 Q9SP15	Q9SP15 macadamia l
3	359	93.5	625	10 Q9SP13	Q9SP13 macadamia l
4	175	45.6	525	10 Q43358	Q43358 theobroma c
5	165	43.0	593	10 Q9SEW4	Q9SEW4 juglans reg
6	119.5	31.1	1038	5 Q60983	Q60983 dictyosteli
7	117	30.5	810	10 Q92W13	Q92W13 cucurbita m
8	117	30.5	1089	12 Q40947	Q40947 kaposi's sa
9	115.5	30.1	554	5 Q9VPS3	Q9VPS3 drosophila
10	111	28.9	1162	12 Q98148	Q98148 kaposi's sa
11	109.5	28.5	1129	12 Q9OR71	Q9OR71 kaposi's sa
12	105	27.3	1390	5 Q77033	Q77033 dictyosteli
13	105	27.3	1737	5 Q9TW28	Q9TW28 dictyosteli
14	104.5	27.2	1590	5 P91152	P91152 caenorhabdi
15	104	27.1	838	5 Q9YOC9	Q9YOC9 dictyosteli
16	103.5	27.0	2701	4 Q9Y520	Q9Y520 homo sapien
17	102.5	26.7	876	11 Q9WU62	Q9WU62 mus musculu
18	101.5	26.4	489	10 Q9SP11	Q9SP11 glycine max
19	100.5	26.2	385	5 Q17909	Q17909 caenorhabdi

20	99.5	25.9	1700	5 Q9VVA9	Q9VVA9 drosophila
21	99.5	25.9	2123	5 Q9US7	Q9US7 dictyosteli
22	99	25.8	523	5 Q22540	Q22540 caenorhabdi
23	99	25.8	1027	4 Q9NS7	Q9NS7 homo sapien
24	99	25.8	1165	4 Q9S819	Q9S819 homo sapien
25	99	25.8	1175	4 Q75172	Q75172 homo sapien
26	99	25.8	1233	11 P97820	P97820 mus musculu
27	99	25.8	1257	4 Q95033	Q95033 homo sapien
28	98.5	25.7	378	2 Q31328	Q31328 homo sapien
29	98.5	25.7	378	2 Q08264	Q08264 borrelia bu
30	98.5	25.7	1268	4 Q9UKD8	Q9UKD8 homo sapien
31	98.5	25.7	1276	4 Q9UKD1	Q9UKD1 homo sapien
32	98.5	25.7	1297	4 Q9UKD9	Q9UKD9 homo sapien
33	98.5	25.7	1305	4 Q9UKD3	Q9UKD3 homo sapien
34	98.5	25.7	1323	4 Q9UKD0	Q9UKD0 homo sapien
35	98.5	25.7	1331	4 Q9UKD4	Q9UKD4 homo sapien
36	98.5	25.7	1333	4 Q60298	Q60298 homo sapien
37	98.5	25.7	1352	4 Q9UKD2	Q9UKD2 homo sapien
38	98.5	25.7	1360	4 Q9UKD5	Q9UKD5 homo sapien
39	98	25.5	648	5 Q9TXB8	Q9TXB8 dictyosteli
40	98	25.5	1057	5 Q9VSK3	Q9VSK3 drosophila
41	98	25.5	1339	11 Q35788	Q35788 rattus norv
42	97	25.3	652	4 Q15410	Q15410 homo sapien
43	97	25.3	800	5 Q9Y102	Q9Y102 drosophila
44	97	25.3	2023	4 Q75557	Q75557 homo sapien
45	97	25.3	2023	4 Q9UND7	Q9UND7 homo sapien

ALIGNMENTS

RESULT 1
Q9SP14 ID Q9SP14 PRELIMINARY: PRT: 666 AA.
AC Q9SP14: 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE VICILIN PRECURSOR.
GN AMP2.
OS Macadamia integrifolia (Macadamia nut).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
OX NCBI_Taxid=60698;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=NOT KNOWN.
RA Marcus J.P., Goulet K.C., Green J.L., Manners J.M.;
RT globulin protein in Macadamia integrifolia.*;
RT Plant J. 0:0-0(1999).
DR EMBL: AF161884; AAD54245.1; -
DR HSSP: P02853; 2PHL.
DR INTERPRO: IPR001113; -
DR PFM: PFM0546; SeedScore=7s; 1.
SQ SEQUENCE 666 AA: 78243 MW: 0ECA22F8710F8A7B CRC64;

Query Match 100.0%; Score 384; DR 10; Length 666;
Best Local Similarity 100.0%; Pred. NO. 5.4e-27;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NRORPQOQYEQCQERCRHETPRHMQCOQRCERYEKERKQOXYEQREDEK 60
DB 117 NRORPQOQYEQCQERCRHETPRHMQCOQRCERYEKERKQOXYEQREDEK 176
QY 61 EERMKEDN 69
DB 177 EERMKEDN 185
RESULT 2
Q9SP15

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ID 09SPL5 PRELIMINARY: PRT: 666 AA.
AC 09SPL5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE VICILIN PRECURSOR.
GN AMP2.
OS Macadamia integrifolia (Macadamia nut).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
OX NCBI_TaxID=60698;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=NUT KERNEL;
RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;
RT "A family of antimicrobial peptides is produced by processing of a 7S
RT globulin protein in Macadamia integrifolia kernels.";
RL Plant J. 0:0-(1999).
DR EMBL: AF161883; AAD54244.1; -.
DR HSSP: P02853; 2PHL.
DR INTERPRO: IPR001113; -.
DR PFAM: PF00546; Seedstore_7s; 1.
SQ SEQUENCE 666 AA: 78217 MW: C752B884B2DF0224 CRC64:

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Query Match 95.6%; Score 367; DB 10; Length 666;
Best Local Similarity 95.7%; Pred. No. 1.7e-25;
Matches 66; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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OY 1 NRORPOOQYEOCCORCORNHETEPHMOCCORCERREYKRRKQKRYEEOOREDEEKY 60
DB 117 NRORPOOQYEOCCORCORNHETEPHMOCCORCERREYKRRKQKRYEEOOREDEEKY 176
OY 61 EERMKEDN 69
DB 177 EERMKEDN 185

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RESULT 3
O9SPL3 PRELIMINARY: PRT: 625 AA.
AC 09SPL3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE VICILIN PRECURSOR (FRAGMENT).
GN AMP2.
OS Macadamia integrifolia (Macadamia nut).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
OX NCBI_TaxID=60698;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=NUT KERNEL;
RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;
RT "A family of antimicrobial peptides is produced by processing of a 7S
RT globulin protein in Macadamia integrifolia.";
RL Plant J. 0:0-(1999).
DR EMBL: AF161885; AAD54246.1; -.
DR HSSP: P02853; 2PHL.
DR INTERPRO: IPR001113; -.
DR PFAM: PF00546; Seedstore_7s; 1.
FT NON_TER 1
SQ SEQUENCE 625 AA: 73586 MW: 415808A89D370296 CRC64:

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Query Match 93.5%; Score 359; DB 10; Length 625;
Best Local Similarity 94.2%; Pred. No. 8.5e-25;
Matches 65; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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OY 1 NRORPOOQYEOCCORCORNHETEPHMOCCORCERREYKRRKQKRYEEOOREDEEKY 60
DB 76 NRORPOOQYEOCCORCORNHETEPHMOCCORCERREYKRRKQKRYEEOOREDEEKY 135

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OY 61 EERMKEDN 69
DB 136 EERMKEDN 144

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RESULT 4
O43358 PRELIMINARY: PRT: 525 AA.
AC 043358;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE VICILIN PRECURSOR.
GN CSV.
OS Theobroma cacao (Cacao).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Malvales; Malvaceae; Theobroma.
OX NCBI_TaxID=3641;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEAVES;
RA MEDLINE=92288309; PubMed=1600151;
RA McHenry L., Fritz P.O.;
RT "Comparison of the structure and nucleotide sequences of vicillin genes
RT of cocoa and cotton raise questions about vicillin evolution.";
RL Plant Mol. Biol. 18:1173-1176(1992).
DR EMBL: X62625; CAA44493.1; -.
DR EMBL: X62626; CAA44494.1; -.
DR HSSP: P02853; 2PHL.
DR MENDEL: 30919; Thecc; 1188; 30919.
DR INTERPRO: IPR001113; -.
DR PFAM: PF00546; Seedstore_7s; 1.
DR PRODOM: PD081059; -. 1.
KW SIGNAL.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 525 VICILIN.
SQ SEQUENCE 525 AA: 60798 MW: 19114CD5C248905D CRC64:

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Query Match 45.6%; Score 175; DB 10; Length 525;
Best Local Similarity 32.4%; Pred. No. 1.7e-08;
Matches 33; Conservative 19; Mismatches 14; Indels 36; Gaps 2;
OY 3 ORDPQOQYEOCCORCORNHETEPHMOCCORCERREYKRRKQKRYEEOOREDEEKY 46
DB 35 ERDPQOQYEOCCORCORNHETEPHMOCCORCERREYKRRKQKRYEEOOREDEEKY 94
OY 47 -----KRYEEOOREDEEKY---EERMKED 68
DB 95 QOQOQREOQOCCORCOWEQYKEQGEHENVHNNKRRSEEE 136

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RESULT 5
Q9SEW4 PRELIMINARY: PRT: 593 AA.
AC 09SEW4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE VICILIN-LIKE PROTEIN PRECURSOR (FRAGMENT).
OS Juglans regia (English walnut).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fagales; Juglandaceae; Juglans.
OX NCBI_TaxID=51240;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. SUNLAND; TISSUE=SOFT TISSUE EMBRYO LINE;
RA Teuber S.S., Jarvis K.C., Peterson W.R., Dandekar A.M., Ansari A.A.;
RT "Identification and cloning of a cDNA encoding a vicillin-like protein,
RT Jug r 2, from English walnut kernel (Juglans regia): a major food

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RESULT	9			
09VPS3	PRELIMINARY;	PTT;	554	AA.
ID	09VPS3			
AC	09VPS3;			
DT	01-MAY-2000 (TREMBlrel. 13, Created)			
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)			
DT	01-JUN-2000 (TREMBlrel. 14, Last annotation update)			
DE	CG2839 PROTEIN (FRAGMENT).			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BERKELEY;			
RX	MEDLINE:20196006; PubMed=10731132;			
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,			
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
RA	Stutten G.G., Wortman J.R., Blanchard M.D., Zhang Q., Chen L.X.,			
RA	Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,			
RA	Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mklos G.L.G.,			
RA	Abvill J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,			
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu U., Beasley E.M.,			
RA	Besson K.Y., Benos P.V., Betman B.P., Bhandal D., Bolshakov S.,			
RA	Botkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,			
RA	Buttis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,			
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,			
RA	de Pablos R., Delcher A., Deng Z., Dey S.A., Dow I., Dietz S.M.,			
RA	Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,			
RA	Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,			
RA	Glodet A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,			
RA	Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegwam C.,			
RA	Jatelli M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,			
RA	Liao X., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,			
RA	Lin X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,			
RA	Mekulov G., Milshina N.V., Moberly C., Morris J., Moshrefi A.,			
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,			
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,			
RA	Palazzo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,			
RA	Reinert R., Remington K., Saunders R.D.C., Scheeler F., Shen H.,			
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,			
RA	Spieler E., Spradling A.C., Stapleton M., Strong R., Sun E.,			
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,			
RA	Wang Z.-T., Wassman D.A., Weinstock K.C., Wu D., Yang S., Yao Q.A.,			
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,			
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhu G., Zhao Q., Zheng L.,			
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Zhu H.O.,			
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:			
RT	"The genome sequence of <i>Drosophila melanogaster</i> ."			
RL	Science 287:2185-2195(2000).			
DR	EMBL; AE003588; AA051469.1; -			
DR	PLAYBASE; FBgn0031273; CG2839.			
DR	INTERPRO; IPR001304; -			
DR	PFAM; PF000059; lectin_C.1.			
DR	PROSITE; PSS0041; C_TYPE_LLECTIN_2; 1.			
DR	NON_TER			
EQ	SEQUENCE 554 AA: 69873 MW: 02966852609FD16 CRC64;			

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Query Match      30.1%; Score 115.5; DB 5; Length 554;
Best Local Similarity 36.6%; Pred. No. 0.0034;
Matches 26; Conservative 22; Mismatches 18; Indels 5; Gaps 2;

OY      3 QRDPPQQLTECCQERQHR-----ETEPRIHQITQQQCEKRYIEKKRQQQRYIEQQREDEE 58
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db 341 EKKKEEEEDEDEKKREINKKEDEERKREERKKEDEERKKEDEERKKEDEERKKEE 400
QY 59 -KYERMKEDD 68
    | | | | | | | |
Db 401 RKEERKKEE 411
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RESULT 10
ID 098148 PRELIMINARY; PRT; 1162 AA.
AC 098148;
DT 01-FEB-1997 (TEMBLrel. 02, Created)
DT 01-FEB-1997 (TEMBLrel. 02, Last sequence update)
DT 01-JUN-2000 (TEMBLrel. 14, Last annotation update)
DE ORF73 HOMOLOG.
OS Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).
OC Vitruus; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=37296;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97048116; PubMed=8892957;
RA Cesarian E., Nador R.G., Bal F., Bohenzky R.A., Russo J.J.,
RA Moore P.S., Chang Y., Knowles D.M.;
RT "Kaposi's sarcoma-associated herpesvirus contains G protein-coupled
RT receptor and cyclin D homologs which are expressed in Kaposi's sarcoma
RT and malignant lymphoma."
RL J. Virol. 70:8218-8223(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97094384; PubMed=8939871;
RA Moore P.S., Bashoff C., Weiss R.A., Chang Y.;
RT "Molecular mimicry of human cytokine and cytokine response pathway
RT genes by KSHV."
RL Science 274:1739-1744(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97121480; PubMed=8962146;
RA Russo J.J., Bohenzky R.A., Chien M.C., Chen J., Yan M., Maddalena D.,
RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
RT "Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus
RT (HHV8)."
RL Proc. Natl. Acad. Sci. U.S.A. 93:14862-14867(1996).
RN [4]
RP SEQUENCE FROM N.A.
RA Russo J.J., Bohenzky R.A., Chien M.C., Chen J., Yan M., Maddalena D.,
RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
RL Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Russo J.J., Bohenzky R.A., Chien M.C., Chen J., Yan M., Maddalena D.,
RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
RL Submitted (MAY-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: U55064; AAC55944.1; -
DR EMBL: U75698; AAC57156.1; -
DR INTERPRO: IPR002017; -
DR SWISSPROT: P162 AA; 135213 MW; 1A72CE01C1CB081C CRC64; -

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Query Match          28.9%: Score 111; DB 12; Length 1162;
Best Local Similarity 31.3%: Pred. No. 0.016; -
Matches    21: Conservative   26: Mismatches   20: Indels     0: Gaps     0:
OY      2 RQRDQGVVLEGGCGRHETPRRMVTCGCGCCERRYENKKRQKRVDEQREDEKYE 61
       :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      660 QQQDDQQDDQDDQDDQDDQDDQDDQDDQDDQDDQDDQDDQDDQDDQDDQDDQDD 739
OY      62 ERMKEED 68
       |:|::|:|
Db      740 EQQQQDD 746

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RESULT 11

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OY      2  RORROROROROCORRKHETPRMIO---TCORRCEKRYEKKKOKKRYEORREDEE 58
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      612  QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 671
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      59  KYERMKKE 67
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      672  QQQQQQQQQ 680
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Query Match      27.3%; Score 105; DR 5; Length 1390;
Best Local Similarity    23.9%; Pred. No. 0.062;
Matches 16; Conservative 30; Mismatches 21; Indels 0; Gaps 0;
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```
Query Match      27.3% Score 105 Db 5 Length 1737;
Best Local Similarity 39.1% Pred. No. 0.074;
Matches 27; Conservative 19; Mismatches 19; Indels 4; Gaps 3;
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OY   1 NRODPOQOYCQCORCORNHETEPHHMOTCCQRCRRRYEKE-KRKQOKRYEQOEDEEK 59
     |  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db   940 NKREEEEKKK--LER-ORKPEEEKXELEROREEKEXELEKRREBELELORKEEEK 996
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```
OY   60 YEERRMEED 68
Db   997 EOERKKEE 1005
```

RESULT	14	
P91152		
ID	P91152	PRELIMINARY; PRT; 1590 AA.
AC	P91152;	
DT	01-MAY-1997 (TREMBLrel. 03, Created)	
DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)	
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)	
DE	SIMILAR TO DROSOPHILA SU(VAR)3-9 PROTEIN.	
GN	CA3E11.3	
OS	Caenorhabditis elegans.	
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae	
CC	Rhabditidae; Pelodermineae; Caenorhabditis.	

